

RESULT 1

AAB13956

ID AAB13956 standard; protein; 1402 AA.

XX

AC AAB13956;

XX

DT 15-JUN-2007 (revised)

DT 16-NOV-2000 (first entry)

XX

DE Neurospora crassa QDE-1 protein.

XX

KW Gene silencing; quelling deficient; qde-1; al-1; BOND_PC;

KW RNA-dependent RNA polymerase;

KW RNA-dependent RNA polymerase [Neurospora crassa]; GO3968.

XX

OS Neurospora crassa.

XX

PN WO200050581-A2.

XX

PD 31-AUG-2000.

XX

PF 16-FEB-2000; 2000WO-IT000048.

XX

PR 22-FEB-1999; 99IT-RM000117.

XX

PA (UYRO-) UNIV ROMA LA SAPIENZA.

XX

PI Macino G, Cogoni C;

XX

DR WPI; 2000-579171/54.

DR N-PSDB; AAA65171.

DR PC:NCBI; gi4803727.

XX

PT Novel polynucleotide encoding a polypeptide which has a silencing
PT activity and comprising a RNA-dependent RNA polymerase domain.

XX

PS Claim 21; Fig 4; 48pp; English.

XX

CC The present sequence is the Neurospora crassa QDE-1 protein. This protein
 CC has gene silencing activity. The qde-1 gene was isolated by mutational
 CC analysis of an al-1 transgenic strain. This strain had an albino
 CC phenotype resulting from post-transcriptional silencing of the endogenous
 CC al-1 gene. Reversion of this phenotype indicated a mutation in a
 CC silencing gene. The silencing gene, qde-1, could then be isolated.
 CC Modulation of qde-1 expression may be used to inactivate genes and to
 CC silence suppression of genes

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
 CC information from BOND.

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SQ Sequence 1402 AA;

Query Match 100.0%; Score 7397; DB 3; Length 1402;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MNPITPRKRNSPVVEIIINRLNNDYNLGLQCVADTTLTTPHRRKELAESDEDFGRHDKIYRA 60
      |||
Db      1 MNPITPRKRNSPVVEIIINRLNNDYNLGLQCVADTTLTTPHRRKELAESDEDFGRHDKIYRA 60

Qy     61 LNFLYWRKDDSLNQAEANFFIEAKAASSNWVPKAHADPDTLPWSKEPPRAATAGQQWALQ 120
      |||
Db     61 LNFLYWRKDDSLNQAEANFFIEAKAASSNWVPKAHADPDTLPWSKEPPRAATAGQQWALQ 120

Qy    121 TVLLEVLNRFMPPPNNTPGRTFGRITLSGSGLSRPTSTNTKRKDEPANVTFADPPKRSLT 180
      |||
Db    121 TVLLEVLNRFMPPPNNTPGRTFGRITLSGSGLSRPTSTNTKRKDEPANVTFADPPKRSLT 180

Qy    181 RSATGPPIHGAAIPLKFPDPVNTGSKRPSLESENLNQCTKRAKGLSDNVAAAAAPPVPI 240
      |||
Db    181 RSATGPPIHGAAIPLKFPDPVNTGSKRPSLESENLNQCTKRAKGLSDNVAAAAAPPVPI 240

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Qy	241	ASALDKVPTRRHANTRDPTATGHRRADQVDSFDTSQGTSYGSSVFSACRHNQSTTQSSFE	300
Db	241	ASALDKVPTRRHANTRDPTATGHRRADQVDSFDTSQGTSYGSSVFSACRHNQSTTQSSFE	300
Qy	301	APPSQPREKRPVDATVFEAGHLIESPSKGRITTKSHIDNQPLSSSSQGETSFSTYYESFPS	360
Db	301	APPSQPREKRPVDATVFEAGHLIESPSKGRITTKSHIDNQPLSSSSQGETSFSTYYESFPS	360
Qy	361	SGGEGAIPEPSRSNGLARSEESARSQVQVHAPVVAARLNIWPKFPKWLHEAPLAVAVEV	420
Db	361	SGGEGAIPEPSRSNGLARSEESARSQVQVHAPVVAARLNIWPKFPKWLHEAPLAVAVEV	420
Qy	421	TRLFMHCKVDLEDESGLKYDPSWSTARDVTDIWKTLYRLDAFRGKPFPEKPPNDVFVTA	480
Db	421	TRLFMHCKVDLEDESGLKYDPSWSTARDVTDIWKTLYRLDAFRGKPFPEKPPNDVFVTA	480
Qy	481	MTGNFESKGSAVVLSAVLDYNPDNSPTAPLYLVKLKPLMFEQGCRLTRRFGPDRFFEILI	540
Db	481	MTGNFESKGSAVVLSAVLDYNPDNSPTAPLYLVKLKPLMFEQGCRLTRRFGPDRFFEILI	540
Qy	541	PSPTSTSPSVPPVVSQKPGAVEEVIQWLMGQHSVLVGRQWRAFFAKDAGYRKPLREFQLR	600
Db	541	PSPTSTSPSVPPVVSQKPGAVEEVIQWLMGQHSVLVGRQWRAFFAKDAGYRKPLREFQLR	600
Qy	601	AEDPKPIIKERVHFFAETGITFRPDVFKTRSVVPAEEPVEQRTEFKVSQMLDWLLQLDNN	660
Db	601	AEDPKPIIKERVHFFAETGITFRPDVFKTRSVVPAEEPVEQRTEFKVSQMLDWLLQLDNN	660
Qy	661	TWQPHLKLFSRIQLGLSKTYAIMTLEPHQIRHHKTDLLSPSGTGEVMNDGVGRMSRSVAK	720
Db	661	TWQPHLKLFSRIQLGLSKTYAIMTLEPHQIRHHKTDLLSPSGTGEVMNDGVGRMSRSVAK	720
Qy	721	RIRDVLGLGDVPSAVQGRFGSAKGMWVIDVDDTGDEDWIETYPQQRKWECDVFDKHQRTL	780
Db	721	RIRDVLGLGDVPSAVQGRFGSAKGMWVIDVDDTGDEDWIETYPQQRKWECDVFDKHQRTL	780
Qy	781	EVRSVASELKSAGLNLQLLPVLEDRARDKVKMRQAIGDRLINDLQRQFSEQKHALNRPVE	840
Db	781	EVRSVASELKSAGLNLQLLPVLEDRARDKVKMRQAIGDRLINDLQRQFSEQKHALNRPVE	840
Qy	841	FRQWVYESYSSRATRVSHGRVPFLAGLPDSQEETLNFMLNSGFDPPKKQKYLQDIAWDLQK	900
Db	841	FRQWVYESYSSRATRVSHGRVPFLAGLPDSQEETLNFMLNSGFDPPKKQKYLQDIAWDLQK	900
Qy	901	RKCDTLKSKLNIRVGRSAYIYMIADFVGWLEENEVHVGFSSKFRDEEESFTLLSDCDVLV	960
Db	901	RKCDTLKSKLNIRVGRSAYIYMIADFVGWLEENEVHVGFSSKFRDEEESFTLLSDCDVLV	960
Qy	961	ARSPAHFPSDIQVRVAVFKPELHSLKDVIIFSTKGDVPLAKKLSGGDYDGDMAWVCWDPE	1020
Db	961	ARSPAHFPSDIQVRVAVFKPELHSLKDVIIFSTKGDVPLAKKLSGGDYDGDMAWVCWDPE	1020
Qy	1021	IVDGFVNAEMPLEPDLNRYLKKDKTTFKQLMASHGTGSAAKEQTTYDMIQKSFHFALQPN	1080
Db	1021	IVDGFVNAEMPLEPDLNRYLKKDKTTFKQLMASHGTGSAAKEQTTYDMIQKSFHFALQPN	1080
Qy	1081	FLGMCTNYKERLCYINNSVSNKPAIILSSLVGNLVDQSKQGIVFNEASWAQLRRELLGGA	1140
Db	1081	FLGMCTNYKERLCYINNSVSNKPAIILSSLVGNLVDQSKQGIVFNEASWAQLRRELLGGA	1140
Qy	1141	LSLPDPMYKSDSWLGRGEPTHIIDYLKFSIARPAIDKELEAFHNAMKAAKDTEDGAHFWD	1200
Db	1141	LSLPDPMYKSDSWLGRGEPTHIIDYLKFSIARPAIDKELEAFHNAMKAAKDTEDGAHFWD	1200
Qy	1201	PDLASYTYFFKEISDKSRSSALLETTLNKRIGEVEKEYGRLVKNKEMRDSKDPYPVRVNQ	1260
Db	1201	PDLASYTYFFKEISDKSRSSALLETTLNKRIGEVEKEYGRLVKNKEMRDSKDPYPVRVNQ	1260
Qy	1261	VYEKWCAITPEAMDKSGANYDSKIRLLELSFLADREMNTWALLRASTAFKLYYHKSPKF	1320

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Db      1261 VYEKWCAITPEAMDKSGANYDSKVIRLLELSFLADREMNTWALLRASTAFKLYYHKSPKF 1320
Qy      1321 VWQMAGRQLAYIKAQMTSRPGE GAPALMTAFMYAGLMPDKKFTKQYVARLEG DGSEYPDP 1380
          |||
Db      1321 VWQMAGRQLAYIKAQMTSRPGE GAPALMTAFMYAGLMPDKKFTKQYVARLEG DGSEYPDP 1380
Qy      1381 EVYEVLGDDDFDGIGFTGNGDY 1402
          |||
Db      1381 EVYEVLGDDDFDGIGFTGNGDY 1402
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